SEQUENCE LISTING

<110> NISHIMURA, Satoru

      KOIKE, Ayumi

<120> CMO gene

<130> PH-744US

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<150> JP 11-273725

<151> 27-SEP-1999

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1828

<212> DNA

<213> Chenopodium album

<220>

<221> CDS

<222> (129)..(1427)

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acatcaat atg gca gca agt gca aca aca atg ttg ctg aaa tac cca aca 170
        Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr
        1   5   10

act gta tgt ggt ata cca aat tca tca tca aac aat gat act tca aat 218
Thr Val Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn
15   20   25   30

aat ata gtc cca att cca caa act agt act aat aat ccg gta ctt aag 266
Asn Ile Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys
                35   40   45

ttt cgt acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct ttt 314
Phe Arg Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe
                50   55   60

cct tct tta aac acc acc act act ccg ccg tcg att caa tca ctt gtc 362
Pro Ser Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val
        65   70   75

cag gaa ttc gat ccg aag att ccg gct aag gat gct ctt acg cct cct 410
Gln Glu Phe Asp Pro Lys Ile Pro Ala Lys Asp Ala Leu Thr Pro Pro
        80   85   90

33

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agc tct tgg tat act gac gct gct ttc tat gct cat gaa ctt gac cgt    458
Ser Ser Trp Tyr Thr Asp Ala Ala Phe Tyr Ala His Glu Leu Asp Arg
95              100             105             110


atc ttt tat aag gga tgg caa gtc cca ggg tac agt gat caa att aag    506
Ile Phe Tyr Lys Gly Trp Gln Val Pro Gly Tyr Ser Asp Gln Ile Lys
                115             120             125


gag cct aac caa tat ttc acc gga acg tta gga aat gtt gaa tat ttg    554
Glu Pro Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu
                130             135             140


gtg tgt cga gat ggt gaa gga aaa gtt cat gca ttt cac aac gtt tgc    602
Val Cys Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys
                145             150             155


acc cat cgt gct tcg att ctt gct tgt gga agt gga aaa aaa tcg tgt    650
Thr His Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys
160             165             170


ttt gtg tgc cct tac cat gga tgg gta ttt ggc atg aat gga tcg ctt    698
Phe Val Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu
175             180             185             190


aca aaa gct tcc aaa gca acc gaa gaa cag tca ctt gat ccc gat gaa    746
Thr Lys Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu
                195             200             205
```

34

ctt ggg ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata ctc   794
Leu Gly Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu
         210   215   220

ata agt ttg gac aga tca agc ctt gaa gta ggt gat gtt gga tct gaa   842
Ile Ser Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu
         225   230   235

tgg ctt ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac cct   890
Trp Leu Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro
         240   245   250

aat tta cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat tgg   938
Asn Leu Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp
255   260   265   270

aag att ttc agt gac aac tat ttg gat agc tcg tac cat gtt cct tat   986
Lys Ile Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr
              275   280   285

gca cac aag tac tat gct act gaa ctc gac ttt gat act tac caa act   1034
Ala His Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr
         290   295   300

gat atg atc gga aac gtc acg att caa aga gtg gca ggg agt tca aac   1082
Asp Met Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn
         305   310   315

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aat ggt ttt aat aga ctt gga tct caa gca ttc tat gct ttt gca tac    1130
Asn Gly Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
    320                 325                 330


cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg cac    1178
Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
    335                 340                 345                 350


att ctt cca tta gga cca agg aaa tgc aaa tta gtg gtg gac tac tac    1226
Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
                355                 360                 365


att gaa aaa tca aag ctg gac gac aag gat tac atc gag aag ggc att    1274
Ile Glu Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
                370                 375                 380


gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa agt    1322
Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
                385                 390                 395


gtc caa aaa ggg ttg gaa aca cca gca tat cgt agt gga aga tat gtg    1370
Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
    400                 405                 410


atg cca att gag aaa gga atc cat cat ttc cac tgc tgg ttg cac caa    1418
Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
    415                 420                 425                 430
```

36

gta ttg aag tgattgcagc agatcatcag atgttcgttt cttcttgtat   1467

Val Leu Lys

tggaattgga tattatgatt aataagtaaa attataatgt cataatgtag ttgagattgt 1527

tgctagagtt gagcgtatgc tcctcatgca ctacttagtt atcaagtgtg tatgtctttg 1587

gtcatgggca aaatgtatgt ttcttgctag aatttatata ttatggtgct aatgtccaat 1647

ataaataaaa accatagcac ccctttaatt ccctacttag gtttatatcc catttatttt 1707

cgggggatct atgagataga ttgtctatga acattatttt tcgactcgtg tatggtattc 1767

atcccttgtg tagggtgaag taaacattga gtgtatgaag ttttcattga gtttctgctt 1827

t   1828

<210> 2

<211> 433

<212> PRT

<213> Chenopodium album

<400> 2

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val

1   5   10   15

Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile

                    20   25   30

Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
                    35   40   45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
                    50   55   60

Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
                65   70   75   80

Phe Asp Pro Lys Ile Pro Ala Lys Asp Ala Leu Thr Pro Pro Ser Ser
                              85   90   95

Trp Tyr Thr Asp Ala Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
                              100   105   110

Tyr Lys Gly Trp Gln Val Pro Gly Tyr Ser Asp Gln Ile Lys Glu Pro
                    115   120   125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
                    130   135   140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
                145   150   155   160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
                              165   170   175

                                          38

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
　　　　　　　180　　　　　　　　　　185　　　　　　　　　190

Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
　　　　　　195　　　　　　　　200　　　　　　　　　205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
　　　　210　　　　　　　　215　　　　　　　220

Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225　　　　　　　　230　　　　　　　235　　　　　　　240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
　　　　　　245　　　　　　　　250　　　　　　　255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
　　　　　　260　　　　　　　265　　　　　　　270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
　　　　　275　　　　　　　280　　　　　　　285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
　　290　　　　　　　295　　　　　　　300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Asn Gly
305　　　　　　　310　　　　　　　315　　　　　　　320

Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr Pro Asn
                325   330   335

Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His Ile Leu
                340   345   350

Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr Ile Glu
                355   360   365

Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile Ala Ile
                370   375   380

Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser Val Gln
385   390   395   400

Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val Met Pro
                405   410   415

Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln Val Leu
                420   425   430

Lys

<210> 3

<211> 1651

<212> DNA

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<213> Chenopodium album

<220>

<221> CDS

<222> (119)..(1423)

<400> 3

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aaattataac aacaaaagga agtgtttagt tattgcttga tcatcatata atatcaac   118

atg tca gca agt gca aca aca atg ttg ctg aaa tac cca aca act gta   166
Met Ser Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
 1   5   10   15

tgt ggt ata cca aat tca tca tca aac aat gat act tca aat aac atc   214
Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
             20   25   30

gtc cca att cca caa act agt act aat aat ccg gta ctt aag ttt cgt   262
Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
         35   40   45

acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct ttt cct tct   310
Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
         50   55   60

tta agt acc acc act act ccg ccg tcg att caa tca ctt gtc cag gaa   358

41

Leu Ser Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65   70   75   80

ttc gat ccg agg att ctg gcc gag gat gct ctc acg cct cct agc tct   406
Phe Asp Pro Arg Ile Leu Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
                85   90   95

tgg tat act gaa cct gcc ttc tat gct cat gaa ctt gac cgt atc ttt   454
Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
                100   105   110

tac aaa gga tgg caa gtc gca ggg tac agc gat caa att aag gag cct   502
Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
        115   120   125

aac caa tat ttc acc gga acg tta gga aat gtt gaa tat ttg gtg tgt   550
Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
        130   135   140

cga gat ggt gaa gga aaa gtt cat gca ttt cac aat gtt tgc act cat   598
Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145   150   155   160

cgt gct tcg att ctt gct tgt gga agt ggc aaa aaa tcg tgt ttc gta   646
Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
                165   170   175

tgc cct tac cat ggt tgg gta ttt ggc atg aat gga tca ctt acg aaa   694

42

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
            180   185   190

gct tcc aaa gca acc gaa gaa cag tcc ctt gat ccc gat gaa ctt ggg   742
Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
        195   200   205

ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata ctc atc agt   790
Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
        210   215   220

ttg gac aga tca agc ctt gaa gta ggc gat gtt gga tct gaa tgg ctt   838
Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225   230   235   240

ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac cct aat ttg   886
Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
            245   250   255

cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat tgg aag att   934
Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
            260   265   270

ttc agt gac aac tac ttg gat agc tcg tac cat gtt cct tat gca cac   982
Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
            275   280   285

aag tac tat gca act gaa ctc gac ttt gat act tat caa acc gat atg   1030

43

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
    290   295   300

att gga aat gtc acg att caa aga gtg gcg ggg agt tca aac aag cca   1078
Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Lys Pro
305   310   315   320

gat ggt ttt gat aga ctt gga tct caa gca ttc tat gct ttt gca tac   1126
Asp Gly Phe Asp Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
                325   330   335

cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg cat   1174
Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
                340   345   350

att ctt cca tta gga cca aga aaa tgc aaa tta gtg gtg gac tac tat   1222
Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
            355   360   365

att gaa aaa tca atg ctg gac gac aag gat tac atc gag aag ggc ata   1270
Ile Glu Lys Ser Met Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
    370   375   380

gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa agt   1318
Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
385   390   395   400

gtc caa aaa ggg ttg gag aca cca gca tat cgt agt gga aga tat gtg   1366

44

```
Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
            405                 410                 415
```

```
atg cca att gag aaa gga atc cat cat ttc cac tgt tgg ttg cac caa    1414
Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
            420                 425                 430
```

```
gta ttg aag tgatagcagc agatcagatg ttcgtttctt aatttccttt           1463
Val Leu Lys
        435
```

```
tattggaact ggataattat aataataata agtaaaaaag taaaattata atgtcatgta 1523

gttgagattg ttgctagagt tgagcgtatg ctcctcatgc acttagttat caagtgtgta 1583

tgtgtttggt catggacaaa atgtttcttg ctagaattta tcatattata aggtgctaat 1643

gtccaata                                                          1651
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<210> 4

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<212> PRT

<213> Chenopodium album

<400> 4

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Met Ser Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
  1               5                   10                  15
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45

Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
              20   25   30

Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
              35   40   45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
              50   55   60

Leu Ser Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65   70   75   80

Phe Asp Pro Arg Ile Leu Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
                  85   90   95

Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
              100   105   110

Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
              115   120   125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
              130   135   140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145   150   155   160

46

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
                165   170   175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
                180   185   190

Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
                195   200   205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
        210   215   220

Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225   230   235   240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
                245   250   255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
                260   265   270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
                275   280   285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
        290   295   300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Lys Pro

47

305   310   315   320

Asp Gly Phe Asp Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
            325   330   335

Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
        340   345   350

Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
        355   360   365

Ile Glu Lys Ser Met Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
    370   375   380

Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
385   390   395   400

Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
                405   410   415

Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
            420   425   430

Val Leu Lys
        435

<210> 5

<211> 1712

<212> DNA

<213> Chenopodium album

<220>

<221> CDS

<222> (133)..(1431)

<400> 5

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tataacatca at atg gca gca agt gca aca aca atg ttg ctg aaa tac cca 171
　　　　　　　　Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro
　　　　　　　　　1　　　　　　　　　5　　　　　　　　　　　　10

aca act gta tgt ggt ata cca aat tca tca tca aac aat gat act tca 219
Thr Thr Val Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser
　　　15　　　　　　　　　　20　　　　　　　　　　25

aat aac atc gtc cca att cca caa act att act aat aat ccg gta ctt 267
Asn Asn Ile Val Pro Ile Pro Gln Thr Ile Thr Asn Asn Pro Val Leu
　30　　　　　　　　　　35　　　　　　　　　　40　　　　　　　　　　45

aag ttt cgt acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct 315
Lys Phe Arg Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala
　　　　　50　　　　　　　　　　　55　　　　　　　　　　60

49

```
ttt cct tct tta aac acc acc act act ccg ccg tca att caa tca ctt    363
Phe Pro Ser Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu
            65                  70                  75
```

```
gtc cag gaa ttc gat ccg agg att ccg gcc gag gat gct ctt acg cct    411
Val Gln Glu Phe Asp Pro Arg Ile Pro Ala Glu Asp Ala Leu Thr Pro
            80                  85                  90
```

```
cct agc tct tgg tat act gaa cct gct ttc tat gct cat gaa ctt gac    459
Pro Ser Ser Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp
            95                  100                 105
```

```
cgt atc ttt tac aag gga tgg caa gtc gca ggg tac agt gat caa att    507
Arg Ile Phe Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile
110                 115                 120                 125
```

```
aag gag cct aac caa tat ttc acc gga acg tta gga aat gtt gaa tat    555
Lys Glu Pro Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr
            130                 135                 140
```

```
ttg gtg tgt cga gat ggt gaa ggt aaa gtt cat gca ttt cac aac gtt    603
Leu Val Cys Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val
            145                 150                 155
```

```
tgc acc cat cgt gct tcg att ctt gct tgt gga agc gga aaa aaa tcg    651
Cys Thr His Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser
            160                 165                 170
```

50

```
tgt ttt gta tgc cct tac cat gga tgg gta ttt ggc atg aat gga tcg      699
Cys Phe Val Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser
    175                 180                 185


ctt aca aaa gct tcc aaa gca agc gaa gaa cag tca ctt gat ccc gat      747
Leu Thr Lys Ala Ser Lys Ala Ser Glu Glu Gln Ser Leu Asp Pro Asp
190                 195                 200                 205


gaa ctt ggg ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata      795
Glu Leu Gly Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile
                210                 215                 220


ctc atc agt ttg gac aga tca agc ctt gaa gta gat gat gtt gga tct      843
Leu Ile Ser Leu Asp Arg Ser Ser Leu Glu Val Asp Asp Val Gly Ser
                225                 230                 235


gaa tgg ctt ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac      891
Glu Trp Leu Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp
            240                 245                 250


cct aat ttg cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat      939
Pro Asn Leu Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn
            255                 260                 265


tgg aag att ttc agt gac aac tat ttg gat agc tcg tac cat gtt cct      987
Trp Lys Ile Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro
270                 275                 280                 285
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51

<400> 6

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
1   5   10   15

Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
            20   25   30

Val Pro Ile Pro Gln Thr Ile Thr Asn Asn Pro Val Leu Lys Phe Arg
            35   40   45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
        50   55   60

Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65   70   75   80

Phe Asp Pro Arg Ile Pro Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
                85   90   95

Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
                100   105   110

Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
                115   120   125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
            130   135   140

54

```
agt gtc caa aaa ggg ttg gag aca cct gcg tat cgt agt gga aga tat      1371
Ser Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr
        400                     405                     410


gtg atg cca att gag aaa gga atc cat cat ttc cac tgt tgg ttg cac  .   1419
Val Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His
        415                     420                     425


caa gta ttg aag tgattgcagc agatcagatg ttcgtttctt aatttccttt          1471
Gln Val Leu Lys
430


tattggaatt ggatgattgt tataataata agtaaaatta taatgtcatg tagttgagat 1531

tgttgctaga gttgagcgta tgctcctcat gcacttagtt atcaagtgtg tatgtgtttg 1591

gtcatgggca aaatgtattt tcttgctaga atttgttata ttatggtgct aatgtccaat 1651

aatataaata acaccattgc accctttccc tacttgagaa attatatccc atttattttc 1711

g                                                                  1712
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<210> 6

<211> 433

<212> PRT

<213> Chenopodium album

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tat gca cac aag tac tat gct act gaa ctc gac ttt gat act tac caa    1035
Tyr Ala His Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln
            290                 295                 300

act gat atg atc gga aat gtc acg att caa aga gtg gca ggg agt tca    1083
Thr Asp Met Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser
            305                 310                 315

aac aat ggt ttt aat aga ctt gga tct caa gca ttc tac gct ttt gca    1131
Asn Asn Gly Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala
            320                 325                 330

tac cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg    1179
Tyr Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met
        335                 340                 345

cac att ctt cca tta gga cca agg aaa tgc aaa tta gtg gtg gac tac    1227
His Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr
350                 355                 360                 365

tat att gaa aaa tca aag ctg gac gac aag gat tac atc gag aag ggc    1275
Tyr Ile Glu Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly
            370                 375                 380

ata gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa    1323
Ile Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu
            385                 390                 395
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52

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145   150   155   160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
               165   170   175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
               180   185   190

Ala Ser Lys Ala Ser Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
               195   200   205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
       210   215   220

Leu Asp Arg Ser Ser Leu Glu Val Asp Asp Val Gly Ser Glu Trp Leu
225   230   235   240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
               245   250   255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
               260   265   270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
               275   280   285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
    290   295   300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Asn Gly
305   310   315   320

Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr Pro Asn
                325   330   335

Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His Ile Leu
            340   345   350

Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr Ile Glu
            355   360   365

Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile Ala Ile
    370   375   380

Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser Val Gln
385   390   395   400

Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val Met Pro
                405   410   415

Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln Val Leu
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Lys

56

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tayttrtgng crtanggnac rtgrta   26

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cccgggttta gttattgctt gatcat   26

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gagctcctgc aatcacttca atactt   26

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taatggatcc attaacgccg tcgc   24

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<223> Synthetic DNA

<400> 14

gggtaccaat cacttcaata cttgg   25

<210> 15

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<212> DNA

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<220>

<223> Synthetic DNA

<400> 15

cccgggaaaa ccattatggc cgtcgc   26

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<220>

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<220>

<221> CDS

<222> (1)..(126)

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Met	Ala	Ala	Ser	Ala	Thr	Thr	Met	Leu	Leu	Lys	Tyr	Pro	Thr	Thr	Val	
1				5					10					15		

tgt	ggt	ata	cca	aat	tca	tca	tca	aac	aat	gat	act	tca	aat	aac	atc	96
Cys	Gly	Ile	Pro	Asn	Ser	Ser	Ser	Asn	Asn	Asp	Thr	Ser	Asn	Asn	Ile	
			20				25					30				

gtc	cca	att	cca	caa	act	att	act	aat	aat	c						127
Val	Pro	Ile	Pro	Gln	Thr	Ile	Thr	Asn	Asn							
		35					40									

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<212> PRT

<213> Artificial Sequence

<400> 17

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
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Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
　　　　　　　　　20　　　　　　　　　25　　　　　　　　　30

Val Pro Ile Pro Gln Thr Ile Thr Asn Asn
　　　　　　　　35　　　　　　　　40

SEQUENCE LISTING FREE TEXT

SEQ ID NO:7:　　n represents a,g,c or t (location: 9).

SEQ ID NO:7:　　n represents a,g,c or t (location: 15).

SEQ ID NO:7:　　n represents a,g,c or t (location: 18).

SEQ ID NO:8:　　n represents a,g,c or t (location: 9).

SEQ ID NO:8:　　n represents a,g,c or t (location: 15).

SEQ ID NO:8:　　n represents a,g,c or t (location: 18).